

Db	61	CITCAVINRQVKVNCATSNAGCGDCLPFRYRKTRIGLQDGPCICPCTKQTPSEVOCAF	RN [1]
Qy	121	QLSLVEADAPTPVPOEQATVALVSSLVWFTLAFLGLFFLYCKQFFNRHQCQGGLOFEA	RP SEQUENCE FROM N.A.
Db	121	QLSLEVEADAPTPVPOEQATVALVSSLVWFTLAFLGLFFLYCKQFFNRHQCQGGLOFEA	RA Chaudhary D., Long A.J.;
Qy	181	DKTAKESLFPVPPSKESAESQVS 205	RT "TRATE", a novel TNF receptor family member associated with death
Db	181	DKTAKESLFPVPPSKESAESQVS 205	RT signalling.;
RESULT 2			RT Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
ID	Q9N2V2	PRELIMINARY; PRT; 423 AA.	DR EMBL; AF245998; AAKB3395_1; -.
AC	Q9N2V2;		DR InterPro; IPR01368; TNFR_C6.
DT	01-OCT-2000 (TREMBIrel. 15, Created)		DR Pfam; PF00020; TNFR_C6; 2.
DT	01-JUN-2001 (TREMBIrel. 17, Last annotation update)		DR SMART; SM00208; TNFR; 2.
DE	TAU-ALPHA.		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
OS	Homo sapiens (Human).		DR PROSITE; PS00050; TNFR_NGFR_2; 1.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		SQ SEQUENCE 417 AA; 45319 MW; 3AA85D7827AB35C4 CRC64;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1]		
RN	CITCAVINRQVKVNCATSNAGCGDCLPFRYRKTRIGLQDGPCICPCTKQTPSEVOCAF		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2020246; PubMed=10809768;		
RA	EDY M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;		
RT	"PAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-Independent Cell Death.";		
RL	J. Biol. Chem. 275:15336-15342(2000).		
DR	EMBL; AE167555; AAFT1828.1; -.		
DR	InterPro; IPR001368; TNFR.		
DR	Pfam; PF00020; TNFR_c6; 2.		
DR	SMART; SM00208; TNFR; 2.		
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		
DR	PROSITE; PS00050; TNFR_NGFR_2; 1.		
SEQUENCE	423 AA; 46071 MW; BB7C9917132A4B2F CRC64;		
SO			
Query Match	38.1%; Score 485; DB 4; Length 423;		
Best Local Similarity	44.4%; Pred. No. 8.1e-44;		
Matches	87; Conservative 29; Mismatches 80; Indels 0; Gaps 0;		
Qy	2 DCOENEWDDQGRGCYVCQRCGPQELSKGDFYKQFFNRHQCQGGLOFEA		
Db	33 DCROQEFDRRSRGNCVPCNQCGPMELSKCGFGYGEDAQCVTCRLHRFKEDWGFOCKPC		
Qy	62 ITCAVINRQVKVNCATSNAGCGDCLPFRYRKTRIGLQDGPCICPCTKQTPSEVOCAF		
Db	93 LDCAVINRFQKANCSATSDAICGDCIPGFRYRKTKLVGFQDMECVPGCQDPPIPYPHEPASK		
Qy	122 LSIVLVEADAPTPVPOEQATVALVSSLVWFTLAFLGLFFLYCKQFFNRHQCQGGLOFEA		
Db	153 VNLVKIATASTASSPRITALAVICSLATVALVLLILTCVICKRQFMEKKPSWSLRSDIQ		
Qy	182 KTKAKESLFPVPPSKE 197		
Db	213 YNGSELSCFDRPQHE 228		
RESULT 3			
ID	Q9NS68	PRELIMINARY; PRT; 423 AA.	
AC	Q9NS68;		
DT	01-OCT-2000 (TREMBIrel. 15, created)		
DT	01-OCT-2000 (TREMBIrel. 15, Last annotation update)		
DE	TREMBIrel. 17, Last annotation update)		
GN	HTROY.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=9606;		
Qy	62 ITCAVINRQVKVNCATSNAGCGDCLPFRYRKTRIGLQDGPCICPCTKQTPSEVOCAF		
Db	93 LDCAVINRFQKANCSATSDAICGDCIPGFRYRKTKLVGFQDMECVPGCQDPPIPYPHEPASK		
Qy	122 LSIVLVEADAPTPVPOEQATVALVSSLVWFTLAFLGLFFLYCKQFFNRHQCQGGLOFEA		
Db	153 VNLVKIATASTASSPRITALAVICSLATVALVLLILTCVICKRQFMEKKPSWSLRSDIQ		
Qy	182 KTKAKESLFPVPPSKE 197		
Db	213 YNETEELSCFDRPQHE 228		
RESULT 4			
ID	Q9NS68	PRELIMINARY; PRT; 423 AA.	
AC	Q9NS68;		
DT	01-OCT-2000 (TREMBIrel. 15, created)		
DT	01-OCT-2000 (TREMBIrel. 15, Last annotation update)		
DE	TREMBIrel. 17, Last annotation update)		
GN	HTROY.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=9606;		
Qy	62 ITCAVINRQVKVNCATSNAGCGDCLPFRYRKTRIGLQDGPCICPCTKQTPSEVOCAF		
Db	93 LDCAVINRFQKANCSATSDAICGDCIPGFRYRKTKLVGFQDMECVPGCQDPPIPYPHEPASK		
Qy	122 LSIVLVEADAPTPVPOEQATVALVSSLVWFTLAFLGLFFLYCKQFFNRHQCQGGLOFEA		
Db	153 VNLVKIATASTASSPRITALAVICSLATVALVLLILTCVICKRQFMEKKPSWSLRSDIQ		
Qy	182 KTKAKESLFPVPPSKE 197		
Db	213 YNETEELSCFDRPQHE 228		
RESULT 5			
ID	Q9BY00	PRELIMINARY; PRT; 417 AA.	
AC	Q9BY00;		
DT	01-JUN-2001 (TREMBIrel. 17, Created)		
DT	01-JUN-2001 (TREMBIrel. 17, Last annotation update)		
DE	TRADEALPHA.		
DR	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
OX			
Query Match	37.9%; Score 493; DB 4; Length 423;		
Best Local Similarity	44.4%; Pred. No. 8.2e-44;		
Matches	87; Conservative 29; Mismatches 80; Indels 0; Gaps 0;		
Qy	2 DCOENEWDDQGRGCYVCQRCGPQELSKGDFYKQFFNRHQCQGGLOFEA		
Db	33 DCROQEFDRRSRGNCVPCNQCGPMELSKCGFGYGEDAQCVTCRLHRFKEDWGFOCKPC		

QY	62	ITCAVINRQVKNCATSNAVGDCPRLPRYKTRIGLQLQDORCIPCTKQTPTSEVOCAFQ	RT : : : : : : : : : : : : : : : : : : receptor superfamily ";		
Db	93	LDCAVVNRFQKANCATSQDAGCGDCPRLPRYKTRIGLQLQDORCIPCTKQTPTSEVOCAFQ	RT Genomics 62:103-107(1999).		
QY	122	LSLVADAPTPVPPQEATLVALVSSLLVFTLAFLGLFLFLYCKQFFNHCQRGGLQFED	RL EMBL: AF13166; AAF19795.1; -.		
Db	153	VNLVKIATASSPRDLALAVICSALATVLVLLILCIVYCYRCQFMERKKPSNLSRQDIO	DR MGD; MGI:1352474; TNFRSF19.		
Qy	182	KTAKEESLFVPPSKE 197	DR Inter-Pro: IPR01368; TNFR_c6; 2.		
Db	213	YNGSELSCFDLRPQLHE 228	DR SMART: SM00208; TNFR; 2.		
			DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		
			DR PROSITE; PS0050; TNFR_NGFR_2; 1.		
			SQ SEQUENCE: 348 AA; 38450 MW; 013C799638F8E333 CRC64;		
			Query Match 37.5%; Score 478; DB 11; Length 348; Best Local Similarity 40.4%; Pred. No. 2. 3e-43; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 0;		
Qy	2	DQQEHEWWDQWGRVCYTCQCPGPQGELSKGDCPRLPRYKSSWGHHKQOSC	Qy 2 DQQEHEWWDQWGRVCYTCQCPGPQGELSKGDCPRLPRYKSSWGHHKQOSC 61		
Db	33	Q9BXZ9; 01-JUN-2001 (TREMBLrel. 17, Created)	Db 33 DCROCALVNRFGRANCSTSADVGCDLPGFYRKTKLGVFQDMBCVPGDPPPPYEPHCTSK 92		
DE		DE TRADEBA.			
DT		DT Homo sapiens (Human).			
OS		OS Homo sapiens (Human).			
OC		OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC		OC NCBI_TAXID=9606;			
OX		OX [1]			
RN		RN SEQUENCE FROM N.A.			
RA		RA Chaudhary D., Long A.J.; TRADE: a novel TNF receptor family member associated with death			
RT		RT Submitted (MAR 2000) to the EMBL/GenBank/DDJB databases.			
RR		RR EMBL: AF246999; AAK21396.1; -.			
DR		DR Inter-Pro: IPR01368; TNFR_c6.			
DR		DR Pfam: PF00020; TNFR_c6.			
SMART		SMART: SM00208; TNFR; 2.			
PROSITE		PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.			
SEQUENCE		SEQUENCE: 423 AA; 45979 MW; 46D5641A8A96BA2 CRC64;			
SQ		SQ SEQUENCE: 423 AA; 45979 MW; 46D5641A8A96BA2 CRC64;			
Query Match	37.7%	Score 480; DB 4; Length 423; Best Local Similarity 49.1%; Pred. No. 1. 7e-43; Matches 81; Conservative 28; Mismatches 56; Indels 0; Gaps 0;	Qy 122 LSLVADAPTPVPPQEATLVALVSSLLVFTLAFLGLFLFLYCKQFFN----- 167		
RT		RT signaling ";	Db 153 VNLVKIATASSPRDLALAVICSALATVLVLLILCIVYCYRCQFMERKKPSNLSRQDIO 212		
RR		RR Submitted (MAR 2000) to the EMBL/GenBank/DDJB databases.	Qy 168 -----RHICORGGLQFED 181		
DR		DR EMBL: AF247000; AAK21397.1; -.	Db 213 YNGSELSCFDQPLRICAHRACCCQFRD 240		
			RESULT 7		
Q9JH6		Q9JH6 PRELIMINARY; PRT; 416 AA.	Q9JH6 PRELIMINARY; PRT; 416 AA.		
ID		ID Q9JH6; 01-OCT-2000 (TREMBLrel. 15, Created)	ID Q9JH6; 01-OCT-2000 (TREMBLrel. 15, Created)		
AC		AC DTRKPFKDSNGCNVCLQKQPMELSKCGFGIEDAQCTVCRHLRFKEDWGFQKCKPC 92	AC DTRKPFKDSNGCNVCLQKQPMELSKCGFGIEDAQCTVCRHLRFKEDWGFQKCKPC 92		
DT		DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT		DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE		DE TROY (TRADE).	DE TROY (TRADE).		
GN		GN TNFRSF19 OR TROY.	GN TNFRSF19 OR TROY.		
OS		OS Mus musculus (Mouse).	OS Mus musculus (Mouse).		
OC		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TAXID		NCBI_TAXID=10090;	NCBI_TAXID=10090;		
[1]		[1]	[1]		
SEQUENCE		SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
RX		RX MEDLINE=20347167; PubMed=10764796;	RX MEDLINE=20347167; PubMed=10764796;		
RA		RA Kojima T., Morikawa T., Copeland N.G., Gilbert D.J., Jenkins N.A., Senba E., Kitamura T.	RA Kojima T., Morikawa T., Copeland N.G., Gilbert D.J., Jenkins N.A., Senba E., Kitamura T.		
RT		RT "TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles";	RT "TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles";		
RT		RT embryonic skin and hair follicles";	RT embryonic skin and hair follicles";		
RL		RL J. Biol. Chem. 275:20742-20747(2000).	RL J. Biol. Chem. 275:20742-20747(2000).		
RN		RN [2]	RN [2]		
RP		RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.		
RC		RC STRAIN=C57BL/6;	RC STRAIN=C57BL/6;		
RA		RA Chaudhary D., Long A.J.; TRADE: a novel TNF receptor family member associated with death	RA Chaudhary D., Long A.J.; TRADE: a novel TNF receptor family member associated with death		
RT		RT signaling ";	RT signaling ";		
RR		RR Submitted (MAR 2000) to the EMBL/GenBank/DDJB databases.	RR Submitted (MAR 2000) to the EMBL/GenBank/DDJB databases.		
RL		RL EMBL: AB00432; BAB03267.1; -.	RL EMBL: AB00432; BAB03267.1; -.		
DR		DR EMBL: B247000; AAK21397.1; -.	DR EMBL: B247000; AAK21397.1; -.		
DR		DR MGD; MGI:1352474; TNFRSF19.	DR MGD; MGI:1352474; TNFRSF19.		
DR		DR Inter-Pro: IPR01368; TNFR_c6.	DR Inter-Pro: IPR01368; TNFR_c6.		
DR		DR SMART: SM00208; TNFR; 2.	DR SMART: SM00208; TNFR; 2.		
DR		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.	DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		
DR		DR SEQUENCE: 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;	DR SEQUENCE: 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;		
Query Match	37.5%	Score 478; DB 11; Length 416;	Query Match	37.5%	Score 478; DB 11; Length 416;

	Best local Similarity 40.4%; Pred. No. 2.8e-43; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;	ID 09JHFL PRELIMINARY; PRT; 214 AA.
QY	2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92	ID 09JHFL PRELIMINARY; PRT; 214 AA.
Db	33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92	AC 09JHFL; DT 01-OCT-2000 (TREMBlrel. 15, Created)
QY	62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121	DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
Db	93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152	DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
QY	122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167	DE TAJ-BETA1.
Db	153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212	GN TNFRSF19.
QY	168 -----RHORGGLQFEAD 181	OS mus musculus (mouse).
Db	213 YNGSELSCFDQPRLRCAHRCACQYHRD 240	OC Mammalia; Bacteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RESULT 8		OX NCBI_TaxID=10090;
Q9JLL3		RN [1]
ID 09JLL3	PRELIMINARY; PRT; 416 AA.	RP SEQUENCE FROM N.A.
AC 09JLL3;		RX MEDLINE=20347167; PubMed=10764796;
DT 01-OCT-2000 (TREMBlrel. 15, Created)		RA Kojima T., Motkawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)		RA Senba E., Kitamura T.,
DE TAJ-ALPHA LONG.		RT "TROY", a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles.";
GN TNFRSF19.		RT J. Biol. Chem. 275:20742-20747(2000).
OS MUS musculus (Mouse).		RL R.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		RN [2]
OX NCBI_TaxID=10090;		RP SEQUENCE FROM N.A.
RN [1]		RX MEDLINE=20270246; PubMed=10809768;
SEQUENCE FROM N.A.		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RX MEDLINE=20270246; PubMed=10809768;		RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent cell Death.",
RX MEDLINE=20270246; PubMed=10809768;		RL J. Biol. Chem. 275:15336-15342(2000).
RX EBY M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;		DR EMBL; AB040433; BAB0368.1; -.
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death.",		DR MGDB; MGJ:135474; TNfrsf19.
RT independent Cell Death.",		DR InterPro; IPR001368; TNFR_c6.
RL J. Biol. Chem. 275:15336-15342(2000).		DR Pfam; PF00020; TNFR_c6; 2.
DR EMBL; AF167552; AAH71825.1; -.		DR SMART; SM00208; TNFR; 2.
DR MGI; MGI:1352474; TNfrsf19.		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR InterPro; IPR001368; TNFR_c6.		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
DR Pfam; PF00020; TNFR_c6; 2.		DR SEQUENCE FROM N.A.
DR SMART; SM00208; TNFR_c6.		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		Query Match
SEQUENCE FROM N.A.		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
Q9JLL2		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
ID Q9JLL2	PRELIMINARY; PRT; 150 AA.	DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
AC 09JHFL; DT 01-OCT-2000 (TREMBlrel. 15, Created)		QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)		DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
DE TAJ-BETA1.		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
GN TNFRSF19.		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
OS mus musculus (mouse).		RT J. Biol. Chem. 275:20742-20747(2000).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bacteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		RN [1]
OX NCBI_TaxID=10090;		RP SEQUENCE FROM N.A.
RN [1]		RX MEDLINE=20270246; PubMed=10809768;
RP SEQUENCE FROM N.A.		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RX MEDLINE=20270246; PubMed=10809768;		RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,"
RA "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death.",		RT independent Cell Death.",
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death.",		RL J. Biol. Chem. 275:15336-15342(2000).
RT independent Cell Death.",		DR EMBL; AB040433; BAB0368.1; -.
RL J. Biol. Chem. 275:15336-15342(2000).		DR MGDB; MGJ:135474; TNfrsf19.
DR InterPro; IPR001368; TNFR_c6.		DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.		DR SMART; SM00208; TNFR; 2.
DR SMART; SM00208; TNFR_c6.		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
DR SEQUENCE FROM N.A.		DR SEQUENCE FROM N.A.
Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
Query Match		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
Best Local Similarity 37.5%; Score 478; DB 11; Length 416; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92		DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
Db 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92	RESULT 10	QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121		DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
Db 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
Db 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
QY 168 -----RHORGGLQFEAD 181		RT J. Biol. Chem. 275:20742-20747(2000).
Db 213 YNGSELSCFDQPRLRCAHRCACQYHRD 240		RN [1]
RESULT 9		RP SEQUENCE FROM N.A.
Q9JHFL		RX MEDLINE=20270246; PubMed=10809768;
RT J. Biol. Chem. 275:20742-20747(2000).		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT independent Cell Death.",		RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,"
RT independent Cell Death.",		RT independent Cell Death.",
RT independent Cell Death.",		RL J. Biol. Chem. 275:15336-15342(2000).
RT independent Cell Death.",		DR EMBL; AB040433; BAB0368.1; -.
RT independent Cell Death.",		DR MGDB; MGJ:135474; TNfrsf19.
RT independent Cell Death.",		DR InterPro; IPR001368; TNFR_c6.
RT independent Cell Death.",		DR SMART; SM00208; TNFR; 2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
RT independent Cell Death.",		DR SEQUENCE FROM N.A.
RT independent Cell Death.",		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
RT independent Cell Death.",		Query Match
RT independent Cell Death.",		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
RT independent Cell Death.",		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
RT independent Cell Death.",		DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
RT independent Cell Death.",		QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
RT independent Cell Death.",		DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
RT independent Cell Death.",		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
RT independent Cell Death.",		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
RT independent Cell Death.",		RT J. Biol. Chem. 275:20742-20747(2000).
RT independent Cell Death.",		RN [1]
RT independent Cell Death.",		RP SEQUENCE FROM N.A.
RT independent Cell Death.",		RX MEDLINE=20270246; PubMed=10809768;
RT independent Cell Death.",		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT independent Cell Death.",		RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,"
RT independent Cell Death.",		RT independent Cell Death.",
RT independent Cell Death.",		RL J. Biol. Chem. 275:15336-15342(2000).
RT independent Cell Death.",		DR EMBL; AB040433; BAB0368.1; -.
RT independent Cell Death.",		DR MGDB; MGJ:135474; TNfrsf19.
RT independent Cell Death.",		DR InterPro; IPR001368; TNFR_c6.
RT independent Cell Death.",		DR SMART; SM00208; TNFR; 2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
RT independent Cell Death.",		DR SEQUENCE FROM N.A.
RT independent Cell Death.",		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
Query Match		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
Best Local Similarity 37.5%; Score 478; DB 11; Length 416; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92		QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
Db 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92	RESULT 10	DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
Db 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
Db 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212		RT J. Biol. Chem. 275:20742-20747(2000).
QY 168 -----RHORGGLQFEAD 181		RN [1]
Db 213 YNGSELSCFDQPRLRCAHRCACQYHRD 240		RP SEQUENCE FROM N.A.
RESULT 9		RX MEDLINE=20270246; PubMed=10809768;
Q9JHFL		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
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RT independent Cell Death.",		DR MGDB; MGJ:135474; TNfrsf19.
RT independent Cell Death.",		DR InterPro; IPR001368; TNFR_c6.
RT independent Cell Death.",		DR SMART; SM00208; TNFR; 2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
RT independent Cell Death.",		DR SEQUENCE FROM N.A.
RT independent Cell Death.",		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
Query Match		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
Best Local Similarity 37.5%; Score 478; DB 11; Length 416; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92		QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
Db 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92	RESULT 10	DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
Db 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
Db 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212		RT J. Biol. Chem. 275:20742-20747(2000).
QY 168 -----RHORGGLQFEAD 181		RN [1]
Db 213 YNGSELSCFDQPRLRCAHRCACQYHRD 240		RP SEQUENCE FROM N.A.
RESULT 9		RX MEDLINE=20270246; PubMed=10809768;
Q9JHFL		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
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RT independent Cell Death.",		DR EMBL; AB040433; BAB0368.1; -.
RT independent Cell Death.",		DR MGDB; MGJ:135474; TNfrsf19.
RT independent Cell Death.",		DR InterPro; IPR001368; TNFR_c6.
RT independent Cell Death.",		DR SMART; SM00208; TNFR; 2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
RT independent Cell Death.",		DR SEQUENCE FROM N.A.
RT independent Cell Death.",		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
Query Match		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
Best Local Similarity 37.5%; Score 478; DB 11; Length 416; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92		QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
Db 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92	RESULT 10	DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
Db 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
Db 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212		RT J. Biol. Chem. 275:20742-20747(2000).
QY 168 -----RHORGGLQFEAD 181		RN [1]
Db 213 YNGSELSCFDQPRLRCAHRCACQYHRD 240		RP SEQUENCE FROM N.A.
RESULT 9		RX MEDLINE=20270246; PubMed=10809768;
Q9JHFL		RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
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RT independent Cell Death.",		DR MGDB; MGJ:135474; TNfrsf19.
RT independent Cell Death.",		DR InterPro; IPR001368; TNFR_c6.
RT independent Cell Death.",		DR SMART; SM00208; TNFR; 2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
RT independent Cell Death.",		DR PROSITE; PS00652; TNFR_NGFR_2; 1.
RT independent Cell Death.",		DR SEQUENCE FROM N.A.
RT independent Cell Death.",		Q9JLL2 23564 MW; ECC63981C37482B8 CRC64;
Query Match		Best Local Similarity 37.2%; Score 474; DB 11; Length 214; Matches 79; Conservative 29; Mismatches 57; Indels 0; Gaps 0;
Best Local Similarity 37.5%; Score 478; DB 11; Length 416; Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92
Matches 84; Conservative 30; Mismatches 66; Indels 28; Gaps 1;		DB 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92
QY 2 DQCENEYWDQGRGCVTCORCGPGQELSKEKGFGYGEDAQCPFRPRKEFQKPCP 92		QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121
Db 33 DCRQEKKDRSGNCVLCRQCGPGMELSKBKGFGYGEDAQCPFRPRKEFQKPCP 92	RESULT 10	DB 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152
QY 62 ITCAVINRQVKNTATSNAVGCGCLPRPYRKTRIGGLQDQECIPCTKQTPSEVOCAFQ 121		QY 122 LSLVEADPTVPPOEATVALVSSLLWVFTLPLGLFLYCKOEN----- 167
Db 93 ADCALVNRFQRANSHTSDAWCCDCLPFRYKRLVKGQDMECVPGDPDPPIEPHCTSK 152		DB 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212
Db 153 VNLYKISSTVSSPRDTALAAVICSALATVLLALLILCIVIYCKRQEMKKPSWSRSQDIQ 212		RT J. Biol. Chem. 275:20742-20747(2000).
QY 168 -----RHORGGLQFEAD 181		RN [1]
Db 213 YNGSELSCFDQPRLRCAHRCACQYHRD 240		RP SEQUENCE FROM N.A.
RESULT 9		RX MEDLINE=20270246; PubMed=10809768;

OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurogaulthi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99364417; PubMed=10311242;
 RA Headon D.J.; Overbeek P.A.;
 RT "Involvement of a novel tnf receptor homologue in hair follicle
 induction.";
 RL Nat. Genet. 22:370-374(1999).
 DR EMBL; AR160502; AD50425.1; -.
 DR MGD; MGI:1343498; Edar.
 DR InterPro; IPR000488; Death.
 DR Pfam; PF00531; death; 1.
 KW Receptor.
 SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;

Query Match 14.4%; Score 183.5; DB 11; Length 448;

Best Local Similarity 25.0%; Pred. No. 1.9e-11; Indels 70; Conservative 29; Mismatches 122; Gaps 59; Matches 13; RT

OY 2 DQ0ENEYWDQ-WGRCVWCQRCGGFQELSKDCGYEGEDAY-CTACPPRYKSSWGHMKCOS 89
 Db 30 NC0GENEYHNOTQNLGCQCPPCRGEPEPMSCCGYGTKDGYCVPCKPRR-----YKSSWG 54
 QY 55 HKCQSCITCAVINRQVKVNCTATSNAVCGDCLPFRYR-KTRIGGLQDQECPCTKQTPT 113
 Db 90 HKDCCEGFRRATVLTGPDM-----DAECGPCLPGYTMLENRPRTNIGMVCYSLAPPN 144
 QY 114 SWQCAFQLSLVEDA-----PTVPROE-----ATVLVALVSSLLVFLAFL 155
 Db 145 TKFECVGATSGYSAHSSSTSGGTSLSPPQHAKHEKLSQGHHLATALLTAMSTIFIMAIV 203
 QY 156 GLFFLY--CKOFNRHCORGGLLOFFADKTAKEES-----LIP-----VPPS 195
 Db 204 LIMFMYIIMTKTFSSAPCCSSPPGKSADAPANHEEKREAPDSVWTPENGEFOKLATPT 263
 QY 196 KEPMSAEQSVWAGPSIAQQLFS---LDSVPIPQQQGPEM 231
 Db 264 KTPPKSENDAS--SENEQLLRSVSDDEEPAKDGQSPEL 300

RESULT 14

O90VY2 PRELIMINARY; PRT; 514 AA.

AC O90VY2; DT 01-DEC-2001 (TREMBlre. 19, created)
 DT 01-DEC-2001 (TREMBlre. 19, last sequence update)
 DE ECTODYSPLASIN-A RECEPTOR.

GN ORyzas latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belioniformes; Adrianichthyidae; Oryziinae; Oryzias.

NCBI_TaxID=8090;

[1]

RP SEQUENCE FROM N.A.

RK Kondo S.; Shima A.;

RT "The medaka rs-3 locus required for scale development encodes ectoysplasin-A receptor";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF364815; AAK83298.1; -.

KW Receptor.

SQ SEQUENCE 514 AA; 56074 MW; 8389E28082798632 CRC64;

Query Match 12.9%; Score 164.5; DB 13; Length 514;

Best Local Similarity 25.5%; Pred. No. 2.5e-09; Indels 56; Conservative 34; Mismatches 103; Gaps 27; RT

OY 3 COENETYWDQGR-CVTCORGPSQELSKDCGYEGEDAY-CTACPPRYKSSWGHMKCOS 60
 Db 32 CGEYEFFNQTSNSOACPCPQGPQEPNMSCHGKMDGECFAVCPQGKY-SKGKEICR 90

QY 61 CITO-AVTRQVKVNCTATSNAVCGDCLPFRYR-KTRIGGLQDQECPCTKQTPT 118
 Db 91 HKDCNALLYKATVREPGTAEKDARCGPCLPGYMMENRARNLYAMVCHSC-QNAPLNTEC 149

QY 119 AFQL-----SLVEDATPVPPQEAETVLAVALVESSLVFLA---FIGLFFLYCK 163
 Db 150 KKTTEPIIKPPINGSTVLPHPGSPGQGHHLATALLTAMSTIFIMAIVLIMFYKA 209

QY 164 OFFNRHCORGGLQFEADKTAKEESLFPVP-----PSKE 197
 Db 210 KPNQQACCSGQVVKAVEOTINKLEDKKDYPDNVVIFPEKE 249

Search completed: October 26, 2002, 21:09:48

Job time : 30 secs

Query Match 13.1%; Score 166.5; DB 13; Length 514;
 Best Local Similarity 24.5%; Pred. No. 1.5e-09; Indels 27; Gaps 9; RT

RT ectodysplasin-A receptor";

RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF364816; AAK83299.1; -.

DR EMBL; AF364814; AAK83297.1; -.

DR Receptor.

RK Kondo S.; Shima A.;

RT "The medaka rs-3 locus required for scale development encodes ectoysplasin-A receptor";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF364815; AAK83298.1; -.

KW SEQUENCE FROM N.A.

SQ SEQUENCE 514 AA; 56066 MW; 82C7F0661EECFB48 CRC64;

Query Match 13.1%; Score 166.5; DB 13; Length 514;

Best Local Similarity 24.5%; Pred. No. 1.5e-09; Indels 27; Gaps 9; RT

RT

RL

DR

DR